

FIGURE 1

GGACTAATCTGTGGGAGCAGT'TTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
 GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACACAGTG
 TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATCTCTACTTTTAGGAGGA
 CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
 CTCCTATTATTCTGGCTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCACACATCGCACT
 GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
 ATGATGATGATGAGGACAACCTCTCTTTTCCAACAAGAGAGCCAAAGAAGCCATTTTTTCCA
 TTTGATCTGTTTCCAATGTGTCCATTTGGATGTGAGTGCTATTACAGAGTTGTACATTTGCTC
 AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTTGATACTCGAATGCTTGATCTTC
 AAAACAATAAAATTAAGGAAATCAAAGAAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
 CTGATCCTGAACAACAACAGCTAACGAAGATTCACCCCAAAGCCTTTCTAACCACAAAGAA
 GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAATACCACCTTAATCTTCCCAAAT
 CATTAGCAGAACTCAGAATTCATGAAAAATAAAGTTAAGAAAAATACAAAAGGACACATTCAAA
 GGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAAACCTCTTGATAAATAATGGGATAGA
 GCCGAGGGCATTGGAAGGGGTGACGGTGTTCCATATCAGAATTGCAGAAGCAAACTGACCT
 CAGTCTCTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
 ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGGCTGGGCTTAGGAAACAA
 CAAAATCACAGATATCGAAAAATGGGAGTCTTGCTAACATACCAGCTGTGAGAGAAATACATT
 TGGAAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
 ATCTTCTTCTATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
 AAAGATGAAGAAATCTTTATACAGTGAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
 AAATGCAACCTGCAACATTTCTGTTGTGTTTGGAGCAGATGAGTGTTTCAGCTTGGGAACCTT
 GGAATGTAATAATTAGTAATTTGGTAATGTCCATTTAATAAAGATTCAAAAATCCCTACATT
 TGGAAATCTTGAACCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA
 AGTGGTAAGTCCACTGACTTATTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
 GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTCTTTTTGCGTACAATGAT
 CTTACATAAATCTCATGCTTGACCATTCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
 TTTAACACCTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
 TAGCAAAATTTGTGCTCTTTCAATTGCTGTTAGAAAAACAGAAATTAACAAAAGACGTAATGT
 GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACTTGGGTAGTACTGTAATATTTTTAAT
 CATCTTAAAGTATGATTGTATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCGT
 CTTTATGTTTAAAACTAATTCTTAAAAATAAGCCCTTCAGTAAATGTTTATTACCAACTTGA
 TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTAATATT
 ACCTGATTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCGCATT
 AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATTTGTTAGGCTATATAACATTGCCAC
 TTCACCTCAAGGAATATTTTGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGAGCCTGGA
 CACTAACCAATCTACACCAAATTGCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA
 CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
 TATAAATGCTCAGAGTCTTTTATGTATTTCTTATTGGCATCAACATATGTAAAAATCAGAAA
 ACAGGGAAATTTTCATTAATAAATATTGGTTTGAAT

0043351.037001

FIGURE 2

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392
<subunit 1 of 1, 379 aa, 1 stop
<MW: 43302, pI: 7.30, NX(S/T): 1
MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCFPGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLPPEL
KYLQIIFLHNSIARVGVNDFCPTVPMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM
```

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCCGCSGACCGGCCCGGCGCCCTCCGCCCTCCGCACTCGCGCTCC
 CTCCTCGGCCCGCTCCGCGCCCTCTCCCTCCCTCTCCCCAGCTGTCCCGTTCCGGTCA**ATG**CGAGCCTCC
 GGCCTCGCGCCGCTGCTGTCTCTCGGGCTGCTGCTGCTCGGCTCCGGCCGCGCCCGCGGCGCCGCGCCAGA
 GCCCCCGTGTCTGCCATCCGTTCTGAGAAGGAGCCGTGCCGTTCCGGGAGCGCGAGGCTGCACCTTCGCGGG
 GAAGGTCTATGCCCTTGGACGAGACGTGGCACCCGGACCTAGGGCAGCCATTCGGGGTGATGCGCTGCGTGTGTG
 CGCTTGCAGGCGCCTCAGTGGGGTCGCCGTACCAAGGGCCCTGCGAGGGTCAGCTGCAAGAACATCAAAACAGA
 GTGCCAAACCCCGCTGTGGGCGAGCCGCGCAGCTGCGCGGACACTGCTGCCAGACCTGCCCCAGGAGCGAG
 CAGTTTCGAGGCGCAGCGCAGCGGCCCTGTCTTTCAGATATCCGCGGACCCGAGAGCTCGAGCTTATAGCGACCG
 CGGGAGCGCAGCGCTGAGGAGCGCCGCGTGGTGACGGCCACACGGACTTCGTGGCGCTGTACAGGGCCGAG
 GTCGCAGGCGGTGGCACGAGCCGAGTCTCGTGTCTGCGCTCTAGCTTCCGCTTCTCTATCTCTACAGGCGGCT
 GGACCGCCTACAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCTTCGAGCCCCACCCA
 AGATGGCCTGGTCTGTGGGTGTGGCGGCGAGTGCCTCGTTGTCTCTGCGGCTCCTTAGGCGAGAACAGCTGCA
 TGTGGCACTTGTACACTCACTACCCCTTCAGGGGAGGCTCGGGGCGCTCTATCCGCGACCGGGCCCTGGCTGC
 AGAGACCTTCAGTGCCATCTGACTCTAGAAGGCCCCCCACAGCAGGCGTAGGGGGCATCACCTGCTCACTCT
 CAGTGACACAGAGGACTCCTTGCACTTTTGTGCTCTTCCGAGGGCTGTGTGAACCCAGGAGTGGGGGACTAAC
 CCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCGAGTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCCA
 GGAACCAAGGCTTTGCTGAGGTGCTGCCCCAACCAGACTGACAGTCCAGGAGATGGACTGGCTGGTGTGGGGAGCTGCA
 GATGCCCTGGAGTGGGCGAGGCGAGGCGAGGCTGCGCATCAGTGGAACATTTGCTCCAGGAAGAGCTGCGACGT
 CCTGCAAAAGTGCTCTTTGTGGGGCTGATGCCCTGATCCCACTCAGACGGGTGCTGCGGGCTCAGCCAGCTTAC
 GCTGCTAGGAAATGGCTCCTGATCTATCAGGTGCAAGTGGTAGGGACAAGCAGTGAAGTGGTGGCCATGACACT
 GGAGACCAAGCTTCACGCGAGGGATCAGCGCACTGTCTGTGCCACATGCTGGACTCAGCCAGGAGGACACAC
 GGCCTGGGTATCTGCCCTGGGCTGGGTGCCCGAGGGGCTCATATGCTGTGCAAGATGGCTTCTCTGAACGT
 GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCGAGTGGCTGCCCTGCCCTACTGTGGGCAATAGCGCCCG
 CCATGACACGCTGCCCTGCCCCCTAGCAGGAGCCCTGGTGTACTACCCCTGTGAAGGCCAAGCAGCAGGCGACGC
 CTGGCTTTCTTGGATACCACTGTCACTTGCATATGAAGTGTCTGCTGGCTGGGCTGGTGGCTCAGAACAAGG
 CACTGTCACTGCCACCTCCTTGGGCTCCTGGAAACGCCAGGCGCTCGGCGGCTGCTGAAGGATTCTATGGCTC
 AGAGGCCAGGGTGTGGTGAAGGACCTGGAGCGGGAAGTGTGCGGCACCTGGCAAAAGGATGGCTCCTCTGAT
 GATCACCAACAGGGTAGCCCCAGAGGGGAGCTCCGAGGGCGAGGTGCACATAGCCAACCAATGTGAGGTGGCGG
 ACTGCGCTGGAGGCGCGCGGGGCCAGGGGGTGCGGGCGTGGGGGCTCCGGATACAGCCTCTGCTGCGCGGCC
 TGTGGTGCCTGGCTCCCGGCCCTAGCGCCCGCCAAACCTGGTGTGCTTGGGGGCGCCGAGACCCCAACATG
 CTCTCTCGAGGGGCGAGCAGCGCCCCACGGGGCTGCTGGGCGCCCAACTACAGCCGCTCTGTCTCACTCTGCAC
 CTGCCAGAGACCAAGGCTGATCTGTGACCCGGTGGTGTGCCACCGCCAGCTGCCGCCACCCGGTGCAGGCTCC
 CGACAGTGTGCCCTGTTTTCCTCTGAGAAACAAGATGTACAGACTTCCAGGCGCTGCAAGCGGCGAGGCGAGG
 AGGAGAGGGCTGCTATTTTGATGGTGACCGAGCTGGCGGGCAGCGGGTACGCGGTGCGACCCCGTTGTGCCCCC
 CTTTGGCTTAATTAAAGTGTGCTGTCTGCACCTGCAAGGGGGGCTAGGAGAGGTGCACTGTGAGAAGGTGCAGTG
 TCCCGGCTGGCTGTGTGCCAGCTGTGCGTGTCAACCCACAGCACTGCTGCAAAACAGTGTCCAGTGGGCTCGGG
 GGCCACCCCGAGCTGGGGACCCCATGCGAGGCTGATGGGCCCGGGGCTGCCGTTTGTGGGCGAGTGGTTC
 AGAGAGTCAGAGCTGGGACCCCTCAGTGCCCCCTTTTGGAGAGATGAGCTGTATACCTGTCAGATGTGGGGCAGG
 GGTGCCCTCACTGTGAGCGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTGCATGCTGTTT
 CCGCTGCACCGGCCACCGCGGCGCCCGAGAGCCAGAAGTATGATCAGAGCTGGAGAAGAGAGCCGAAGGCTCT**TA**
GGGAGCAGCCGAGAGGCCAAAGTGAACAAGAGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGGAGCTTCTT
 GCATCTCTGTGGGAAGCCAGTGCCTTGTCTCTGTCTGTCTTCACTCCACCCCACTACCTCTGGGAA
 CCACAGCTCCAGAGGGGAGAGGAGCTGGGCGAGAGGTCACAGGTCACCAAGTCACTGCTCTGCCACCC
 TCGGCTCTGTCTGGAAGCCCCACCTTCTCTCTGTACATAATGTCACTGGCTTGTGGGATTTTAAATTA
 TCTTCACTCAGCACCAAGGGGCCCCGACACTCACTCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAG
 TTTTGTATTATTAATAAATTTCTTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MFPSLPAPPAPLLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHFDLQQPFQVMRCVLCACEAPQWGRRTGPGRVSCNLIKPECFTPACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDGHTDFVALLTGPRSQAVAR
ARVSLLSRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLTHPSGEVWGVLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTVQEMD
WLVLGELQMALEWAGRPLGRISGHIAARKSCDVLSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKEPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGSGEQGTVAHLLGPPGTPGPRRLKGFYGSQAQGVVKDLEPELLR
HLAKGMSLMTITTKGSPRGELRGQVHIANQCEVGLRLAAGAGBVRALGAPDTASAAPPVV
PGLPALAPAKPGGPRPRDNPNTCFEQQRPHGARGWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHVQAPDQCCPVCEKQDVRLDPLGPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPPF
GLIKCAVCTCKGGTGEVHCEKVQCPRACAQPVVRNPTDCKKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSVPPFGEEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

[illegible][illegible]

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANFVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSTCTPAGISGANCLVADPCASNPCHHGNCSSSSSSSDGYLCICN
EGYEGNPCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSPFVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGVLLEEMALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSC TCEEYVGTFC EEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCLDPCRNGATCISSLSGFTQCCEPGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAFCLNAATCRDLVNGYECVCLA EYKGT HCELYKDPCANVSLNGATC
DSDGLNGTICAPGFTGEECDIDINECDNPNCHHGGSCLDQPNGYNCHCPHGWWGANCEIHL
QWKS GHMAESLTNMPRHSYIIIGALCVAFILMLIILIVGICRISRIEYQGS SRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

DECEMBER 1987

CTCTGGAAGGTCACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTTCAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGTTTGTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTAACT
CTGGTGGTGGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTACGCAAAATGACTTGGAGTGTTC
AGGAAAAGGAAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACTCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAAC
GCGAGCTGTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGAGAG

09434360

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCTTTT CAGGCTTTT CAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTTATGTGTTTGTGAATGATTCTGTGACTAAGTCTATTTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGT CAGCACTGTGTGCCGGGGGAGAGT CACGCAAATGACTTTGAGTGTTC
AGGAAAAGGAAAAATGCACCAGAAAGCCGT CAGAGGCAACTTTTTCTGTACTCTGTGAGGAGC
AGTACGTGGGTACTTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATATCTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATGATGGGAG

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCGGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA
GCTCCGCTAAGGGCTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCACTCGGCTGCCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATCCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGTCCTGATAGAGGAGTTGTGTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCTTGGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQAALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSPYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIBELLSRGWSEBELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACTATAAATATTCCGGATTATTATACACGTCGCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATCGGGGACTTCCCCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGTCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGCTCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTTCGTGAAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAGAGTACAGGAAGAAAAAATAATGGCAAAGCCCCCTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCAGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTACTGAGATTTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTACACATGCCACCGTGCCAGCACCTGA
ACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACC

[illegible]

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYPAPSTTLLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRRLRDGLVGAQFW SAYVPCQTQDRDALRLTLEQIDILIRMCASYSLELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKF IGIGGDYDAGAKFPQGLE
DVSTYFVLIEELLSSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHDLSRLRQRQSLTSGQELTEIP IHWTAKLPAKWSVSESSPHDPHTHTCPPCPAPELLGGP
SVFLFPKKPKDT
```

[illegible]

FIGURE 14

><ss.DNA38113
><subunit 1 of 1, 422 aa, 1 stop
><MW: 46302, pI: 9.42, NX(S/T): 6
MPAGRRGPAAQSAARRPPLLLPLLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQGDNTECE
YHTVGPHSCHIPKDALFLTPYEIWVEATNRLGSARSVDLTLDILDVVTTDPPPDVHVSrvGG
LEDQLSVRWVSPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRWMMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAACGCTCGCAGCCACAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTATTCTCTAA
 GAGGAGAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
 CTGGACATGTCTCGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGTCTGTGTTGGA
 TTTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCTCAATTTCTGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCGACTGAGCAGAAGATG
 ATTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
 CCTGGCAGTTTTAAAAAGAAAAATCAGTGTTAAGTTTGATGCAGTTATGGATATAAAATGA
 AAGCGCAATAAAGCACCTAGTTTTTCTGAAAACGATTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTTAATGTTGAACTTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
 TCATTTTTGAGGCTTTGGCAGTCTTCATTTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
 CCAAAATGACTTTATTAATAATAATTTCCAAGATTATTTGTTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGTGATTGCACTTAAATTTGT
 ATAATTTGTGTTTCTTTTCTGTCTACATAAAATCAGAAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTCAAAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCGAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AA

GAGGAGAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLILLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIIVTASAAGHVSVPELLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKPDAVIGYKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAACAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTCTGC
TGCTCCTGGGCTGGCGGCCGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCCGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCGCGACGGCGCGACGGCGCGCCCGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGCGGGACCCGCGGGG
CCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGCCCAAGCCAGCCTCGCTCTCGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGTGACGGTGGGTGTGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTTCGGTGTACTCCGA
CTGGCACAGCTCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCTGCTCCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGTCTCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCTCGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGCGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGTCTGTGCGTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGACAGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACAGGCCTTACCA
GTTTTGCCTTTTGGGCAGCCTGACAACACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGGCCAGAC
CCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLALLVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSLSLAQLAQAARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCASAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRNLNISTCH
CHCPPGYTGRCQVRCSLQCVHGRFREEECSCVCDIGYGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFwig
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLAAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGP GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCGCCATGCTCTGCTGCTGGGGCTGTGCCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAACCAAACCTTTGATGACAGAATTTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTTCATCACCACCTTCACTATGC
TTATTGGAGACAAGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGG
GTAAAAAGAGAAAAGGAATAAAACCAAGAAAGAAATGGAGAGAGGGGACTGAAATATTGAG
AGCTTCTGCAGTGATTCAGCAAGGACAAAGCCGCTTTTCTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCTGGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCTCGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCGCTCCCAT
CTACTGTCAATTAACCAAAATGAAACATTTGCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAAATGGAATTTTGGGAGACTTTATCATAGATATGACGTCATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGTCTCTA
AAGACCTTCTCTTTACCCAAGAATGTGGTATTCTGTGCTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGCGAGACCAAGGATGCCCTCTTCACAATTCCTCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTTGGATTTCACACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGATGGGAAAGTGATTCACCATATGTCAACCACCTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCTCAACAAGTACGTGGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCCCAGG
TCGGGGAGACGCACACCCTCAAGATCTTCAACAACCCCGAGAGGCGCGCCGAGGCCAAGTC
TGCATCTTCAACATTGGCATCGGCAACGACGTGGACTCAGGCTGTGGAGAAACTGTCTGCT
GGAGAACTGTGGCTCACACGGCGCTGCACGAGGAGGAGCAGCAGGCTCCAGCTCATCG
GGTCTACGATGAAATCAGGACCCCGCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCGAGGCCACCAAGACCTGTTCGCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCTGAAGACAGATGTGCTGTGCGGCCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCTGGAGGCGATGGAGAGGGGACACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCACAAGGAGCTGCTGAGCTCTTGCTGCAAAGTGACGATGAACCTGC
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCG
TTCACCTCCATGAAGCTGAGGGGGCCGCTCCACGCATGGATGGCTGGAGGAGGCCACGG
CATGTCTGGCTGCCATGGGACCCGAACCGTGGTGCAGAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCCGTCAAAAAAACAACAAAAACAAAAAAGA
CATGGGAGAGATGTTGTTTTCTCTCCACCACCTGGGGATACGATGGAAGATGGCCACCT
CCAAGCCAGGAAGACGGCCCTCACCAGACCATGTCTGCTGGCACCTTGATCTTGGACCTC
CCAGCTTCAGAACTGTGAGAAATAAATGTGTTTTGTTAAGCTAAAAAATAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIIS
RYAFTTVSCRMNLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYPNGSEII IAGKLVDKRLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVGTG
SPRPGDGEGEDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQAQALAVSYRFLTPPTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKFPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

0369

CGGACGCGTGGGGTGCCCCGACATGCGCAGTGTAGTGTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGGCGGCGCCTCCCGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACAGCTCTGTGATTACAGTACTGAA
TCCCAACACGGCAGACCATTATTTACAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACAGCTCGGTTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGACGCCACGACTATCAGGTGGTTCCAA
GGGAACACAGAGACTAAAGGCCAATCGGAGTGGGAAGATGGTGCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCCCTCGGCTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTTGGGTGAGAGTCGATG
ATGAAATGCCCTCAACACGCCGTAAGTGTCTGGGCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATATCCCTCCTCCCAACAACAACCACCACCA
CCACCACCACCACCACCATTCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCGGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTTCTGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGTGGCCGATGACGCGACGACGACGACATATAATCAATGCAGAAGGA
GGACAGAACCAACTCCGAAGAAAAGAGGACTACTTCATCTAGATCAGCCTTTTGTTCCTAAT
GAGGTGTCCAACCTGGCCCTATTAGATGATAAAGAGACAGTGATATTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPQRQTIYFRDPRPLKDSRFQLLNFSSELKVSITNSISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTLKG
KSEVEEWSDMYTVTSQMLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMT
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTIITDSRAGEEGSIRAVDH
AVIGGVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAAACGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA
 CCGCGCAGGAAAGACTGAGGCCGCGGCTGCCCGCCGGCTCCCTGCGCCGCGCGCGCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
 GGGGCTCGGGGTGACGGGCTGCCATCCGGCTGCCAGTGACAGCCACAGACAGTCTTCT
 GCACTGCCCGCCAGGGGACCACGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
 GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCGGGCTGCGGGGCTGCA
 GCTCTGGACTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGCCTGCTGCTGCTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCTGGACACTGCCAACGTGGAG
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGGC
 CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACACCCGATTGCCAGCTGCGGCC
 GAGGACCTGGCCGGCTGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
 CTTGCTGGCGACCTCTCGGGCTCTTCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC
 CCTTCAACTGCGTGTGCCCTTGGCTGGTTTGGCCCCCTGGGTGCGGAGAGCCACGTCA
 CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGTCGCGCTGCTCCT
 GGAGCTTGACTACGGGACTTTGGCTGCCAGCCACCAACACAGCCACAGTGCCACCA
 CGAGGCCGTGGTGGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCTACCTGGCTTAGC
 CCGACAGCGCGGCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCC
 TGTCCCCCAGCCAGGACTGCCACCGTCCACCTCAACTGAGGGGACATGCCACCTGG
 GGACACGGCACCACTGGCGTGTGTGTGCCCGAAGGCTTACGGGCTGTACTGTGAGAGC
 CAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTACGCGGAGGCCACCAACGGTCCCT
 GACCTGGGCATCGAGCCGTGAGCCCCACCTCCCTGCGCTGGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
 AAGCGGCTGGTGACCTGCGACTGCCTGCCTCGCTCGTGAGTACAGGTACCCAGCTGCG
 GCCAACGCCACTTACTCCGTCTGTGTATGCTTTTGGGGCCCGGGCGGTGCGCGAGGGC
 AGGAGGCTGCGGGGAGGCCATACACCCCGCCGCTCCACTCCAACACGCCCCAGTCACC
 CAGGCCCGCAGGGCAACCTGCGCTCCCTCATGCGCCCGCCTGGCCCGGTGCTCCTGGC
 CGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGGGGGGCGGGCCATGGCAGCAGCGG
 CTCAGGACAAGGGGAGGTGGGGCCAGGGGCTGGGCCCTGGAACTGGAGGAGTGAAGTGC
 CCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGGCCTGCCAGCGGGTCTGA
 GTGTGAGGTGCCACTCATGGGCTTCCAGGGGCTGGCCTCCAGTCAACCCCTCCACGCAAGC
 CTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCGGGCTCTCAGCCAGTGAGATGGC
 CAGCCCCCTCCTGTGCCACACCAGTAACTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
 CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGACCTCGGTCTCCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGATGCTATGAGGACAGTGT
 CCGCCCTGCCCTCCGCAACCTGAGTCCCTGGGCACGGCGGGCTGTCATGTGCTGGTAAAC
 GCATGCTGGGCCCTGCTGGGCTCTCCCACTCCAGCGGACCTGGGGGCCAGTGAAGGAAG
 CTCGCCGAAAGAGCAGAGGGAGAGCGGGTAGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
 AAGCAAGGAACAAAGAACTGAAAGGAAGATGCTTTAGGAACATGTTTGTCTTTTAA
 AATATATATATATTTATAAGAGATCCTTTCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
 AGAGACAAGGACTTTGGTTTTTGTAAAGCAAACGATGATATGAAGGCCTTTTGTAAAGAAAA
 ATAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPVPRDVPDPTVGLYVFEN
GITMLDASSFAGLPGLQLDLSQNIASRLRLPRLLLDLSHNSLLALEPGILDANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWSPTAP
ATEAPSPPTAPPTVGVPVQPDCCPPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTLGIEPVSPSLRVGLQRYLQGSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPLGPGRVPEGEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAGVAAAYCVRGRAMAAAAQDKQGVGPGAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGLQSPHLAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAACCACAGCTGTTGGCAGGGTCCCCAGCTCATGCCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCCAGAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTCACCATGGGTCAGGTGGTGTCTCAGAAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCGGACCGGGCTTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTACACCAAGGGGATATTCTGAGTGTCTAATATCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACTGTGATT
GTGTTATAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGGAATGTGCAGGAACAGAGGCATCTTCCTGGGTTTGGCTC
CCCGTTCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFL LAPKGP PGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRRAVL TQKQKKQHSVLHVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTFLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACTTCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCCTCTGCTCTGTT
TCCTTCAACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGCAGGAAGATGGGC
TCCCGTGGACAGGGACTTGTGTGGGTACTGCTGCTCTTGGCTTTGCTCTGGCCTGGT
CCTGAGTCTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTCCGCTCCGACCATGCCAGAGGGCTGAAGAAACAACATGAAAAATACAGGCCCATGTAG
GACCAAGGGCTCCCTGCTTCCGGTGTCTGCGTGTCTGTGACCCCGTACCTCCATGTACCC
GGCGACCGCGGTGCCCCAGATCAACATCACTATCTTGAAAGGGGAGAAGGGTGAACGCGGAG
ATCGAGGCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACATGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGGTGGGCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTACCCGGCAAGTTCCTACTGCTAC
GTGCGCGGCTCTACTTCTTTCAGCCTCAACGTGCACACCTGGAAACGAGAAGGAGACCTACCT
GCACATCATGAAGAACGAGGAGGAGGTGGTGATCTTGTTCCGCGAGGTGGGCGACGAGCA
TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCCTC
TACAAGGGCAACCTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATACCTTCAG
TGGTACCTGGTCAAGCACGCCACCGAGCCCTAGCTGGCCGGCCACCTCTTCTCTCGCC
ACCTTCCACCCCTCGCTGTGCTGACCCACCGCTCTTCCCGGATCCCTGGACTCCGACTC
CTTGGCTTTGGCATTTCAGTGAGACGCCCTGCACACAGAAAGCCAAAGCATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGCACCCGC
GAGAACCCTCTGGGACCTTCGCGGCCCTCTGTGCACACATCTCAAGTGACCCCGCAGCGG
GAGACGCGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCCGCGCTCCAGTCTCTTGGAAATA
ATTAGGCAAAATTCTAAAGGTCTCAAAGGAGCAAAAGTAAACCGTGGAGGACAAAGAAAAGGG
TTGTTATTTTGTCTTTCCAGCAGCCTGCTGGCTCCCAAGAGGAGGACCTTTTCAGTTGAG
ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTCTGGGGTCAGGGGAGGGGCGGGGGCAGG
AAACTACCTCTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTCTTGAGGAGATAGGTGAGCC
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTCTGAGTCAGAGCTGCGACCT
GATGGGGGTCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCCGAGGGCTCTGACAGTGGCCAGGACCCCTGGGTCCCCCA
GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCCATGCTCCGACCTGGCACCTGGCATCGGT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCCCTTGGCTCTGTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCTCGTGGGCTAAGCATACCGCTT
CCACGTGTGTGTGGTTGGTGAGCAAGGCTGATCCAGACCCCTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTGTCTGTCTTCTCAGGCTCTGTGAGCATCAGTCTGT
AGACCAGATCAAGAGGAAGTACACGTCCCAATCACCCGTGTAGGATTCACCTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCGTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGGC
GTGTCTCCACGGTGTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCCCTCTCACCTCACCCATGTTGATGCCAGGGTCACTTGTCTGCTACCCGTGGGCC
CCCAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCACACTGGTCTTGTGACTACCTGCG
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTAAAGAACCTT
CTGCGGCTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAACACTGAAATGTGTTTCAA

CCGCTTCTCCCTCTCTTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCAGAGAC

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELSPDPDHAERAEEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGRDRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGAPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGTCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTTCGGGGGAGAGGGAG
 CTGTGACTTACACTTTGGTAATAATTGCTTCTGACACTAAGGCTGTCTGTCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCACTCTTTCTTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATCTTGTCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTTCGACACTCGAAAAACAGCTA
 GACAAACCACTGCTACCTATTTTCTGTCCCAACGAGGAAGCTGTCCATTGAAACACGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGTCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGTGCTCGTGAATAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCACGACCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTGAAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACITTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAAACGTCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGCTGCTTCCCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGACAGGAACGTTACTCAAGACTGGAT
 TATTTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTGCCCAGGCTGGAGTGCAAGTACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTGGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGAATCTTTTAAACCTTAT
 CCAGATGTAGTTCTTCCAATTAATAATTTGAATAAATCTTTTGTACTCAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MPFGEGSLTYTLVIIICFLTRLSASQNCLKKSLEDVVIDIQSSLSKGI RNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQALLAYKEKGHSQSSQFSSDQIEAHLLPENVSALPATVAVASPHSTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCTGGGTACCTGCTCGCAGAGCTCATTCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTGAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAATGAATGGAAATCTTAAAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125